

FIGURE 1

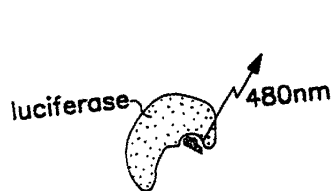


FIGURE 2A

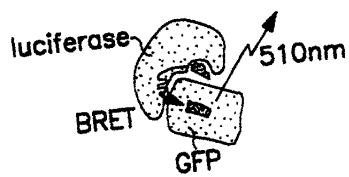


FIGURE 2C

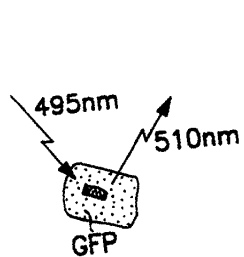


FIGURE 2B

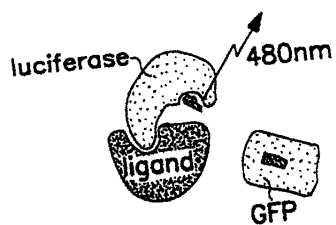


FIGURE 2D

FIGURE 2

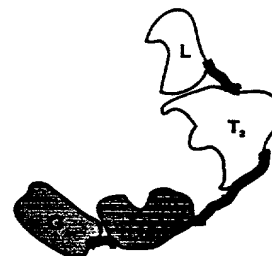
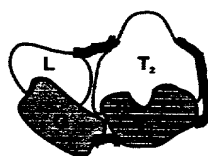
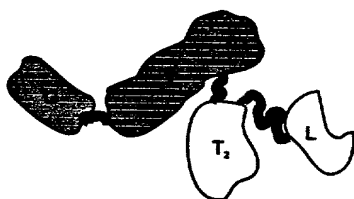
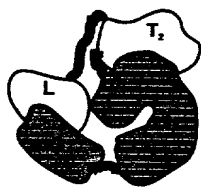
15°

37°



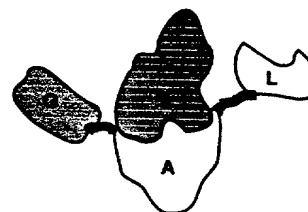
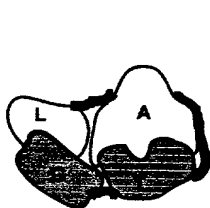
optimized energy transfer module

simple conformational change



complex conformational change

association/dissociation



small molecule interference

large molecule interference



luciferase



GFP



protein domain



antibody fragment



small molecule

BRET sensors are depicted for permissive and non-permissive binding states of the target molecules. Binding may be modulated by varying temperature or ionic strength.

FIGURE 3

## Utilization of advantageous GFP surfaces with substituted fluorophores

	60	*	80	
RM-GFP	:	GAPLPFAFDIVSPA	FQYGNRTFTKYPNDIS--	: 83
Pt-GFP	:	GGPLPFAFDIVSIA	FQYGNRTFTKYPDDIA--	: 83
RR-GFP	:	GAPLPFAFDIVSVA	FSYGNRAYTGYPEEIS--	: 80
cFP484	:	GAPLPFSYDILSNA	FQYGNRALT	KYPDDIA-- : 83
drFP583	:	GGPLPFAWDILSPQ	FQYGSKVYVKHPADIP--	: 80
asFP595	:	GGPLPFAFHILST	SCMYGSKTFIKYVSGIP--	: 77
dsFP483	:	GGPLPFGWHILCP	QFQYGNKAFVHHPDNIH--	: 80
amFP486	:	GGPLAFSFDILST	VFQYGNRCFTAYPTSMP--	: 82
zFP506	:	GGPLPFAEDILSAA	FNYGNRVFTEYPQDIV--	: 80
zFP538	:	GGPLPFESEDILS	AGFKYGDRI	FTEYPQDIV-- : 80

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FIGURE 4

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R_reniform : ---MDLAKLGLKEVMPKINLEGLVGDHAFSMEGVGEGCNILECTQEVKISVTKGAPLPFAFDIVSV : 60
R_mullerei : MSKQI.KNTC.Q...SY.V...I.NN.V...T...C.K...F.N.L.Q.R...P : 63
Ptilosarcu : MNRNV.KNT...I.SA.ASV...I.NN.V...F.K...V.F.N.LMQ.R...G...I : 66
drFP583 : ---.RSS.NVI...F.RF.VRM...T.NG.E.FI...E...RPY...HNT..LK...G...W...L.P : 63

R_reniform : AFSYGNRAYTGYPEEISDYFLOSPFEGFTYERNIRYQDGGTAIVKSDISLEDGKEIVNVDFKAKDL : 120
R_mullerei : .Q...TF.K.K...ND...I...A...M...TL..E...LVEIR...N.IED...VYR.EY.GSNF : 129
Ptilosarcu : .Q...TF.K.K...DD.A...V...A...F...L.FE...AIVDIR...D...D...HYK.EYRNGF : 132
drFP583 : Q.Q...SKV.VKH...AD.P...KKL...K...VMNFE...VVT.TQ.S...Q..C...YK.K.IGVNF : 129

R_reniform : RRMGPVWQODIVGCMQPSYESSMYTNVTSVI GECIIAFKIQTCGHFTYHMRVTYKSKKPVEITMELYHF : 180
R_mullerei : PDD...KT.L...IE...F.A...M.NGVIV...V.LVY...NS...YYSC..K.LM...GV.KEF.S... : 195
Ptilosarcu : PSN...KA.L...E...F.VV...M.SGVIV...VDLVY...ES...NYYS...K.F.R...GG.KEF.E... : 198
drFP583 : PSD...KKTM...WEA...T...RL...PRDGVLK...IHK.L...KD...G.YLVEFKSI.MA...APVQL.G.YY : 195

R_reniform : IQHRLVKTNVDTASGYVVOHETALAAHSTIKKIEGSLP--- : 220
R_mullerei : ...E..Y.EDGGF-E...E...QMTS.G.PL...HEWV : 233
Ptilosarcu : .H...E..Y.EEG.F-E...E...QLT..G.PL...HEWV : 238
drFP583 : VDSK...DI...SHNEDYTI...E..Y...RTEGR.HLFL----- : 226

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FIGURE 5

Aequorea : ---MSKGEELFTGVVILVELDGVNKHKFSVSGEGEDATYKGLTLKFICTT---GKLPFPWPTLVTTFSYGVQCFSRYPDHMK : 79  
R\_mullerei : MSKQILKNTCLQEVMSYKVNLEGJVNHHVFTMECCGKNILFGNQLVQIRVTK--GAPLPFAFDIVSPAQYGNRTFTKYPNDI : 82  
Ptilosarcu : MNRNLKNTGLKEIMSAKASVEGJVNHHVFTMEGFGKGNVLFNGNQLVQIRVTK--GGPLPFAFDIVSPAQYGNRTFTKYPNDI : 82  
R\_reniform : ---MDLAKLGLKEVMPKINLEGJVNHHVFTMEGFGKGNVLFNGNQLVQIRVTK--GAPLPFAFDIVSPAQYGNRTFTKYPNDI : 79  
drFP583 : ---MRSSKNVIEFMRFKVRMEGJVNHHVFTMEGFGKGNVLFNGNQLVQIRVTK--GGPLPFAFDIVSPAQYGNRTFTKYPNDI : 79  
drFP593 : ---MSCSKNVIKFKVRMEGJVNHHVFTMEGFGKGNVLFNGNQLVQIRVTK--GGPLPFAFDIVSPAQYGNRTFTKYPNDI : 79  
dsFP483 : ---MSCSKSVIKREMLIDLHLEGTNCHYFFIKGKKGQPNEGTNTVILEVTK--GGPLPFWHILCPQYQGNKAFVHHPDNI : 79  
cFP484 : ---KALTGMVVIKPDMMKIKLMEGNNVNHAFVIEGEGEPYDGTHTLNLEVKMAEGAPLPFSYDILSNAPQYGNRALTKYPDDI : 82  
asFP595 : ---MASFLAKTMPFKTIEGJVNHHVFTMEGFGKGNVLFNGNQLVQIRVTK--GGPLPFAFDIVSPAQYGNRTFTKYPNDI : 76  
amFP486 : ---MALSNKFIKDDMKWTYHMDQVNGHYFTVKGEGNKPVEGTQTSFTKVTMANGGLPFAFDILSTVFKYGNRCFTAYPTSM : 81  
zFP538 : ---MAHSKHGLKEEMTKYHMEGJVNHHVFTMEGFGKGNVLFNGNQLVQIRVTK--TINLCVIEGGPLPFAFDILSAGFKYGNRTFTKYPNDI : 79  
zFP506 : ---MAQSKHGLKEEMTKYHMEGJVNHHVFTMEGFGKGNVLFNGNQLVQIRVTK--AINLCVIEGGPLPFAFDILSAGFKYGNRTFTKYPNDI : 79

Aequorea : RHDFKFSAMPEGVQERTIFRFDGCKNTRAEVKFEG--DTLVNRIRLGRGIDFEDGNILGHKLEYNNSHNVITIMADKQNGIK : 162  
R\_mullerei : SDYFIQSFPAQFMYERTILRYEDGGJVEIRSDINLIE--DKFYVVEIKVNGNFPDGGVPMQKTI--LGIEPSEAMYM--NNGVIV : 161  
Ptilosarcu : ADYFVQSFPAQFMYERNLREDEGALVIRSDINLIE--DKFYVVEIKVNGNFPDGGVPMQKTI--LGIEPSEAMYM--NNGVIV : 161  
R\_reniform : SDYFLQSFPAQFMYERNIRYQDGGJNIVKSDISLED--GKFIYVNDKAKDLRRMGPMQKTI--VMTSVI : 158  
drFP583 : PDYKLSFPEGPKWERNMNEDEGGVWVTVQDSSLQD--GCFIYVVEIKVNGNFPDGGVPMQKTI--MGWEASSESLYP--RDGVILK : 158  
drFP593 : PDYKLSFPEGPKWERNMNEDEGGVWVTVQDSSLQD--GCFIYVVEIKVNGNFPDGGVPMQKTI--MGWEASSESLYP--RDGVILK : 158  
dsFP483 : HDYKLSFPEGPKWERNMNEDEGGVWVTVQDSSLQD--GCFIYVVEIKVNGNFPDGGVPMQKTI--MGWEASSESLYP--RDGVILK : 158  
cFP484 : ADYFKQSFPEGPKWERNMNEDEGGVWVTVQDSSLQD--GCFIYVVEIKVNGNFPDGGVPMQKTI--MGWEASSESLYP--RDGVILK : 161  
asFP595 : PDYFKQSFPEGPKWERNMNEDEGGVWVTVQDSSLQD--GCFIYVVEIKVNGNFPDGGVPMQKTI--MGWEASSESLYP--RDGVILK : 155  
amFP486 : PDYFKQSFPEGPKWERNMNEDEGGVWVTVQDSSLQD--GCFIYVVEIKVNGNFPDGGVPMQKTI--MGWEASSESLYP--RDGVILK : 160  
zFP538 : VDYFKNSCPAGVTWGRSFLFEDGAVICQNVDTITVSVKENCYHESKPIGAVNFPDGGVPMQKTI--MGWEASSESLYP--RDGVILK : 162  
zFP506 : VDYFKNSCPAGVTWGRSFLFEDGAVICQNVDTITVSVKENCYHESKPIGAVNFPDGGVPMQKTI--MGWEASSESLYP--RDGVILK : 162

Aequorea : VNEKIRHNIEDGSQLADHYQNTPIG-DGPVLLPNNHILSTQALSQDPNEKRDHMLIEFVTAAGITHGMDLYK--- : 238  
R\_mullerei : GEVILVYKLSNGNYTSCMKTIKSKG--VVKFPPSTHFIQHRLEKTYVEDGGF--VEQHETATAQMTSICKPLGSLHEWV : 238  
Ptilosarcu : GEVILVYKLSNGNYTSCMKTIKSKG--GVKEFPEHFIQHRLEKTYVEDGGF--VEQHETATAQMTSICKPLGSLHEWV : 238  
R\_reniform : GEVILVYKLSNGNYTSCMKTIKSKG--PVETMPIHFIQHRLEKTYVEDGGF--VEQHETATAQMTSICKPLGSLHEWV : 233  
drFP583 : GEVILVYKLSNGNYTSCMKTIKSKG--APVQLPGTYVWDSKLDITSHNEDYT--IVEQYERTIEGRHILF--- : 226  
drFP593 : GDTHMALRLEGGHYLVVEFKSYVMVKK--PSVQLPGTYVWDSKLDITSHNEDYT--IVEQYERTIEGRHILF--- : 230  
dsFP483 : GDTHMALRLEGGHYLVVEFKSYVMVKK--AAALMPGTYVWDSKLDITSHNEDYT--IVEQYERTIEGRHILF--- : 232  
cFP484 : GDTHMALRLEGGHYLVVEFKSYVMVKK--KVKLPDTHMDHRIETINHDKDYN--KVTLYENAVARYSLPSQA--- : 231  
asFP595 : QQSILMALKCPGGHILCHLHTVRSKPPASALKMPGTHMDHRIETINHDKDYN--KVTLYENAVARYSLPSQA--- : 232  
amFP486 : GDVTAFLMLQGGNVRCCFHTSNTK--KPVTPMPEHVEHRIARTDLDKGN--SVQLTEHVAHITSVPEF--- : 229  
zFP538 : GDVSMYLLKDKGGRVRCQFDTVYAK--SVPSKMPENHFIQHRLEKTYVEDGGF--VEQHETATAQMTSICKPLGSLHEWV : 231  
zFP506 : GDVSMYLLKDKGGRVRCQFDTVYAK--SVPRKMPDNEFIQHRLEKTYVEDGGF--VEQHETATAQMTSICKPLGSLHEWV : 231

D,E,H,K,R N,Q,S,T L,I,V,M,F,Y,W A,G C,P  
polar charged polar uncharged non-polar hydrophobic small not grouped  
☐ dimerization ☐ hydrophilic  
☐ surfaces ☐ hydrophobic

FIGURE 6